GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM protein - protein search, using sw model

Run on: September 1, 2006, 14:01:07 ; Search time 41 Seconds
                                  (without alignments)
                                  1206.230 Million cell updates/sec

Title: US-10-031-496D-5-PRO8
Perfect score: 2825
Sequence: 1 MYRKLAVpSAFLATARAQSA..........TVCASGTTCQVLNPYYSQCL 514

Scoring table: BLOSUM62
                 Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   PIR_80:*
                 1: pir1:*
                 2: pir2:*
                 3: pir3:*
                 4: pir4:*

                        GenCore version 5.1.9
                 Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM protein - protein search, using sw model

Run on: September 1, 2006, 13:57:45 ; Search time 303 Seconds
                                  (without alignments)
                                  1569.168 Million cell updates/sec

Title: US-10-031-496D-5-PRO8
Perfect score: 2825
Sequence: 1 MYRKLAVpSAFLATARAQSA..........TVCASGTTCQVLNPYYSQCL 514

Scoring table: BLOSUM62
                 Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   UniProt_7.2:*
                 1: uniprot_sprot:*
                 2: uniprot_trembl:*

OM protein - protein search, using sw model

Run on: September 1, 2006, 13:57:06 ; Search time 198 Seconds
                                    (without alignments)
                                    1186.915 Million cell updates/sec

Title: US-10-031-496D-5-PRO8
Perfect score: 2825
Sequence: 1 MYRKLAVpSAFLATARAQSA.........TVCASGTTCQVLNPYYSQCL 514

Scoring table: BLOSUM62
                Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   A_Geneseq_8:*
                 1: geneseqp1980s:*
                 2: geneseqp1990s:*
                 3: geneseqp2000s:*
                 4: geneseqp2001s:*
                 5: geneseqp2002s:*
                 6: geneseqp2003as:*
                 7: geneseqp2003bs:*
                 8: geneseqp2004s:*
                 9: geneseqp2005s:*
                 10: geneseqp2006s:*

                    GenCore version 5.1.9
                Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM protein - protein search, using sw model

Run on: September 1, 2006, 14:06:16 ; Search time 49 Seconds
                                    (without alignments)
                                    918.178 Million cell updates/sec

Title: US-10-031-496D-5-PRO8
Perfect score: 2825
Sequence: 1 MYRKLAVpSAFLATARAQSA.........TVCASGTTCQVLNPYYSQCL 514

Scoring table: BLOSUM62
                Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

```
Database :            Issued_Patents_AA:*
                      1: /EMC_Celerra_SIDS3/ptodata/2/iaa/5_COMB.pep:*
                      2: /EMC_Celerra_SIDS3/ptodata/2/iaa/6_COMB.pep:*
                      3: /EMC_Celerra_SIDS3/ptodata/2/iaa/7_COMB.pep:*
                      4: /EMC_Celerra_SIDS3/ptodata/2/iaa/H_COMB.pep:*
                      5: /EMC_Celerra_SIDS3/ptodata/2/iaa/PCTUS_COMB.pep:*
                      6: /EMC_Celerra_SIDS3/ptodata/2/iaa/RE_COMB.pep:*
                      7: /EMC_Celerra_SIDS3/ptodata/2/iaa/backfiles1.pep:*


                         GenCore version 5.1.9
                   Copyright (c) 1993 - 2006  Biocceleration Ltd.


OM protein - protein search, using sw model

Run on:               September  1, 2006, 14:18:12 ; Search time 181 Seconds
                                             (without alignments)
                                             1315.428 Million cell updates/sec

Title:                US-10-031-496D-5-PRO8
Perfect score:        2825
Sequence:             1 MYRKLAVpSAFLATARAQSA.........TVCASGTTCQVLNPYŸSQCL 514

Scoring table:        BLOSUM62
                      Gapop 10.0 , Gapext 0.5

Searched:             2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters:        2097797

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :            Published_Applications_AA_Main:*
                      1: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
                      2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
                      3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
                      4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
                      5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
                      6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_PUBCOMB.pep:*


                         GenCore version 5.1.9
                   Copyright (c) 1993 - 2006  Biocceleration Ltd.


OM protein - protein search, using sw model

Run on:               September  1, 2006, 14:18:56 ; Search time 33 Seconds
                                             (without alignments)
                                             1072.748 Million cell updates/sec

Title:                US-10-031-496D-5-PRO8
Perfect score:        2825
Sequence:             1 MYRKLAVpSAFLATARAQSA.........TVCASGTTCQVLNPYYSQCL 514

Scoring table:        BLOSUM62
                      Gapop 10.0 , Gapext 0.5

Searched:             250042 seqs, 68872936 residues

Total number of hits satisfying chosen parameters:        250042
```

```
Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :       Published_Applications_AA_New:*
          1:  /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
          2:  /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
          3:  /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
          4:  /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
          5:  /EMC_Celerra_SIDS3/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
          6:  /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
          7:  /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US11_NEW_PUB.pep:*
          8:  /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US60_NEW_PUB.pep:*


                    GenCore version 5.1.9
            Copyright (c) 1993 - 2006  Biocceleration Ltd.



OM protein - protein search, using sw model

Run on:          September  1, 2006, 13:32:11 ; Search time 196 Seconds
                                          (without alignments)
                                          1199.027 Million cell updates/sec

Title:           US-10-031-496D-5
Perfect score:   2822
Sequence:        1 MYRKLAVISAFLATARAQSA.........TVCASGTTCQVLNPYYSQCL 514

Scoring table:   BLOSUM62
                 Gapop 10.0 , Gapext 0.5

Searched:        2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters:      2589679

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :       A_Geneseq_8:*
          1:  geneseqp1980s:*
          2:  geneseqp1990s:*
          3:  geneseqp2000s:*
          4:  geneseqp2001s:*
          5:  geneseqp2002s:*
          6:  geneseqp2003as:*
          7:  geneseqp2003bs:*
          8:  geneseqp2004s:*
          9:  geneseqp2005s:*
          10:  geneseqp2006s:*


                    GenCore version 5.1.9
            Copyright (c) 1993 - 2006  Biocceleration Ltd.



OM protein - protein search, using sw model

Run on:          September  1, 2006, 13:41:20 ; Search time 50 Seconds
                                          (without alignments)
                                          899.815 Million cell updates/sec
```

Title: US-10-031-496D-5
Perfect score: 2822
Sequence: 1 MYRKLAVISAFLATARAQSA.........TVCASGTTCQVLNPYYSQCL 514

Scoring table: BLOSUM62
               Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries

Database :   Issued_Patents_AA:*
          1: /EMC_Celerra_SIDS3/ptodata/2/iaa/5_COMB.pep:*
          2: /EMC_Celerra_SIDS3/ptodata/2/iaa/6_COMB.pep:*
          3: /EMC_Celerra_SIDS3/ptodata/2/iaa/7_COMB.pep:*
          4: /EMC_Celerra_SIDS3/ptodata/2/iaa/H_COMB.pep:*
          5: /EMC_Celerra_SIDS3/ptodata/2/iaa/PCTUS_COMB.pep:*
          6: /EMC_Celerra_SIDS3/ptodata/2/iaa/RE_COMB.pep:*
          7: /EMC_Celerra_SIDS3/ptodata/2/iaa/backfiles1.pep:*

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM protein - protein search, using sw model

Run on: September 1, 2006, 13:53:38 ; Search time 175 Seconds
                              (without alignments)
                            1360.528 Million cell updates/sec

Title: US-10-031-496D-5
Perfect score: 2822
Sequence: 1 MYRKLAVISAFLATARAQSA.........TVCASGTTCQVLNPYYSQCL 514

Scoring table: BLOSUM62
               Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries

Database :   Published_Applications_AA_Main:*
          1: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
          2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
          3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
          4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
          5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
          6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_PUBCOMB.pep:*

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM protein - protein search, using sw model

Run on: September 1, 2006, 13:54:00 ; Search time 33 Seconds
                                         (without alignments)
                                         1072.748 Million cell updates/sec

Title: US-10-031-496D-5
Perfect score: 2822
Sequence: 1 MYRKLAVISAFLATARAQSA.........TVCASGTTCQVLNPYYSQCL 514

Scoring table: BLOSUM62
                 Gapop 10.0 , Gapext 0.5

Searched: 250042 seqs, 68872936 residues

Total number of hits satisfying chosen parameters: 250042

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Published_Applications_AA_New:*
           1:    /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
           2:    /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
           3:    /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
           4:    /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
           5:    /EMC_Celerra_SIDS3/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
           6:    /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
           7:    /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US11_NEW_PUB.pep:*
           8:    /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US60_NEW_PUB.pep:*

                      GenCore version 5.1.9
                 Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM protein - protein search, using sw model

Run on: September 1, 2006, 13:36:09 ; Search time 42 Seconds
                                         (without alignments)
                                         1177.510 Million cell updates/sec

Title: US-10-031-496D-5
Perfect score: 2822
Sequence: 1 MYRKLAVISAFLATARAQSA.........TVCASGTTCQVLNPYYSQCL 514

Scoring table: BLOSUM62
                 Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   PIR_80:*
           1:    pir1:*
           2:    pir2:*
           3:    pir3:*
           4:    pir4:*

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM protein - protein search, using sw model

Run on: September 1, 2006, 13:32:44 ; Search time 302 Seconds
                                          (without alignments)
                                          1574.364 Million cell updates/sec

Title: US-10-031-496D-5
Perfect score: 2822
Sequence: 1 MYRKLAVISAFLATARAQSA..........TVCASGTTCQVLNPYYSQCL 514

Scoring table: BLOSUM62
                 Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   UniProt_7.2:*
                 1: uniprot_sprot:*
                 2: uniprot_trembl:*